

GM50005

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Figure 1 [SEQ ID NO:2]

1 MLNLENKTYV IMGLANKRSI AFGVAKVLDQ LGAKLUVFTYR KERSRKELEK
51 LLEQLNQPEA HLYQIDVQSD EEVINGFEQI GKDVGNIDGV YHSIAFANME
101 DLRGRFSETS REGFLLAQDI SSYSLTIVAH EAKKLMPEGG SIVATTYLGG
151 EFAVQNYNVM GWAKASLEAN VKYLAIDLGP DNTRVNAISA GPIRTLSAKG
201 VGGFNTILKE IEERAPLKRN VDQVEVGKTA AYLLSDLSSG VTGENNIHVDS
251 GFHAIK

Figure 2 [SEQ ID NO: 1]

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1 ATGTTAAATC TTGAAACAA AACATATGTC ATCATGGAA TCGCTAATAA
51 GCGTAGTATT GCTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA
101 AATTAGTATT TACTTACCGT AAAGAACGTA GCGGTAAAGA GCTTGAAGAA
151 TTATTAGAAC AATTAAATCA ACCAGAACGG CACTTATATC AAATTGATGT
201 TCAAAGCGAT GAAGAGGTAA TTAAATGGTT TGAGCAAATT GTAAAGATG
251 TTGGCAAAAT TGATGGTGTAA TATCATTCAA TCGCATTGCTA TAATATGGAA
301 GACTTACGCC GACGCCCTTC TGAAACCTCA CGTGAAGGCT TCTTGTAGC
351 TCAAGACATT AGTTCTTACT CATAACAAAT TGTGGCTCAT GAAGCTAAA
401 AATTAAATGCC AGAAGGTGGT AGCATTGTTG CAACAAACATA TTAGGTGGC
451 GAATTCCAG TTCAAAATTA TAATGTGATG GGTGTGCTA AAGCGAGCTT
501 AGAAGCAAAT GTAAATATT TAGCATTAGA CTTAGGTCT CATAATATTG
551 GCGTTAATGCA ATTTCAGCT GGTCCTAAATCC GTACATTAAG TGCAAAAGGT
601 GTGGGTGGTT TCAAATACAAAT TCTTAAAGAA ATCGAACAGGC GTGCACCTTT

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Figure 2A

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651 AAAACGTAAC GTTGATCAAG TAGAAGTAGG TAAAACAGCG GCTTACTTRT
701 TAAGTGACTT ATCAAGTGGC GTTACAGGTG AAAATATTCA TGTAGATAGC
751 GGATTCCACG CAATTAAATA A